

Figure 1. Translated sequence of human PAP- $\alpha$ 1 cDNA.

CCTGTGGGAGAGAGCGCCGGATCCGGACGGGGTAGCAACCAGGGCAGGCCGTGCCGGCTGA	62
GGAGGTCTGAGGCTACAGAGCTGCCGGCTGGCACACGAGCGCCTCGGCACCAACCGA	122
GTGTTCGCGGGGCTGTGAGGGGAGGGCCCCGGCGCCATTGCTGGCGGTGGAGCGCCG	182
CCCGGTCTCAGCCCCCTCGCTCTCCCTCCGGCTGGGAGGGCCGTATCTCGG	242
GGCCGTCGCCAGCCCCGGCCGGCTCGATAATCAAGGGCCTCGGCCGTCGCCCCGACC	302
TCATTCCATCGCCCTTGCCGGGAGCCGGCAGAGACC ATG TTT GAC AAG ACG	356
Met Phe Asp Lys Thr	
5	
CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
10 15 20	
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA	446
Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln	
25 30 35	
CGA GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA	491
Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys	
40 45 50	
GAA GAC ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA	536
Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro	
55 60 65	
TTC AGT ATT ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC	581
Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr	
70 75 80	
TGT AAC CTT TTG CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA	626
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile	
85 90 95	
GCC ACT ATT TAC AAA GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT	671
Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala	
100 105 110	
GCT AGT CAG TCC CTG ACT GAC ATT GCC AAG TAT TCA ATA GGC AGA	716
Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg	
115 120 125	
CTG CGG CCT CAC TTC TTG GAT GTT TGT GAT CCA GAT TGG TCA AAA	761
Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys	
130 140	
ATC AAC TGC AGC GAT GGT TAC ATT GAA TAC TAC ATA TGT CGA GGG	806
Ile Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly	
145 150 155	
AAT GCA GAA AGA GTT AAG GAA GGC AGG TTG TCC TTC TAT TCA GGC	851
Asn Ala Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly	
160 165 170	
CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG TTT GTG GCA CTT TAT	896
His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr	
175 180 185	
CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA CTC TTA CGC CCC	941
Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro	
190 195 200	
ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT GTG GGC CTT	986
Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr Val Gly Leu	
205 210 215	
TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG TTG ACT	1031
Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Leu Thr	
220 225 230	
GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA TAT	1076
Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val Tyr	
235 240 245	
GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA	1121
Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys	
250 255 260	

Continuation of Figure 1.

GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG	1166
Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly	
265 270 275	
AAT CAC TAT CCG AGC AAT CAC CAG CCT TGA AAG GCAGCAGGGTGCCAG	1215
Asn His Tyr Pro Ser Asn His Gln Pro ***	
280	
GTGAAGCTGGCTGTTCTAAAGGAAAATGATTGCCACAAGGCAAGAGGATGCATCTT	1275
CTTCCTGGTGTACAAGCCTTAAAGACTTCTGCTGCTGATATGCCCTTGATGCACACT	1335
TTGTGTGTACATAGTTACCTTAACTCAGTGGTTATCTAATAGCTCTAAACTCATTAAAA	1395
AAACTCCAAGCCTCCACCAAAACAGTCCCCACCTGTATACATTTTATTAAAAAATG	1455
TAATGCTTATGTATAAACATGTATGTAATATGCTTCTATGAATGATGTTGATTAAAT	1515
ATAATACATATTAAAATGTATGGGAGAACCAAAAAAAAAAAAAAA	1563

Figure 2. Translated sequence of human PAP- $\alpha$ 2 cDNA

CCTGTGGGAGAGAGCGCCGGGATCCGGACGGGGTAGCAACC	62
GGAGGTCTGAGGCTACAGAGCTGCCGCCGCTGGCACACGAGC	122
GTGTCGCCGGGGCTGTGAGGGAGGGCCCGGGCATTGCTGGC	182
CCCGGTCTCAGCCGCCCTCGCTGCTCTCCTCCGGCTGGGA	242
GGCCGTCGCCAGCCCCGGCCCGCTCGATAATCAAGGGCTCG	302
TCATTCCATCGCCCTTGCCGGGCAGCCGGCAGAGACC ATG	356
Met Phe Asp Lys Thr	
5	
CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC	401
Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys	
10 15 20	
TCC ATG CCT ATG GCT GTT CTA AAA TTG GGC CAA	446
Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln	
25 30 35	
CAG AGA GGC TTT TTC TGT AAA GAC AAC AGC ATC	491
Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile	
40 45 50	
CAT GAC AGT ACC GGC GGA TCC ACT GTC CTC ATC	536
His Asp Ser Thr <u>Ala</u> <u>Ala</u> Ser Thr Val Leu	
55 60 65	
GGC TTG CCC GTT TCC TCT ATT ATT CTT GGA GAA	581
Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu	
70 75 80	
TAC TGT AAC CTT TTG CAC TCA AAT TCC TTT ATC	626
Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile	
85 90 95	
ATA GCC ACT ATT TAC AAA GCC ATT GGA ACC TTT	671
Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe	
100 105 110	
GCT GCT AGT CAG TCC CTG ACT GAC ATT GCC AAG	716
Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys	
115 120 125	
AGA CTG CGG CCT CAC TTC TTG GAT GTT TGT GAT	761
Arg Leu Arg Pro His Phe Leu Asp Val Cys Asp	
130 135 140	
AAA ATC AAC TGC AGC GAT GGT TAC ATT GAA TAC	806
Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Tyr	
145 150 155	
GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG TTG	851
Gly Asn Ala Glu Arg Val Lys Glu Gly Arg Leu	
160 165 170	
GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG	896
Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu	
175 180 185	
TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA	941
Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala	
190 195 200	
CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC	986
Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser	
205 210 215	
CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG	1031
Leu Ser Arg Val Ser Asp Tyr Lys His His Trp	
220 225 230	
ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA	1076
Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile	
235 240 245	
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT	1121
Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser	
250 260	

Continuation of Figure 2

AAA GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT	1166
Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr	
265 270 275	
GGG AAT CAC TAT CCG AGC AAT CAC CAG CCT TGA AAGGCAGCAGGGTGCC	1215
Gly Asn His Tyr Pro Ser Asn His Gln Pro ***	
280 285	
CAGGTGAAGCTGGCCTGTTCTAAAGGAAAATGATTGCCACAAGGCAAGAGGGATGCATC	1275
TTTCTTCCTGGTGTACAAGCCTTAAAGACTTCTGCTGCTGATATGCCTCTGGATGCAC	1335
ACTTTGTGTGTACATAGTTACCTTAACTCAGTGGTTATCTAATAGCTCTAAACTCATTA	1395
AAAAAACTCCAAGCCTTCCACCAAAACAGTGCCCCACCTGTATACATTTTATTAAAAAA	1455
ATGTAATGCTATGTATAAACATGTATGTAATATGCTTCTATGAATGATGTTGATTAA	1515
AATATAATACATATTAAAATGTATGGGAGAACCAAAAAAAAAAAAAAAA	1566

D E S S E N D E R - D I F F U S E

Figure 3. Translated sequence of PAP- $\beta$  cDNA

GGCGCAGCTCTGCAAAAGTTCTGCTCGGGATCTGGCTCTTCCCCTGGACTTAGAACG	62
ATTAGGGTTGACAGAGGAAAGCAGAGGCCGCAGGAGGAGCAGAAAACACCACCTTCTG	122
CAGTTGGAGGCAGGCAGCCCCGGCTGCACTCTAGCCGCCGCAGCCGGAGCCGGGCCGAC	182
CCGCCACTATCCGCAGCAGCCTCGGCCAGGAGGCGACCCGGCGCTGGGTGTGGCTG	242
CTGTTGCGGGACGTCTCGCGGGGGAGGCTCGCGGCCAGCCAGCGCC ATG CAA	299
	Met Gln
AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC	344
Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly	
5 10 15	
GGC AGC CCG GCG CTC AAC AAC CCG AGG AGG AGC GGC AGC AAG	389
Gly Ser Pro Ala Leu Asn Asn Pro Arg Arg Ser Gly Ser Lys	
20 25 30	
CGG GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG	434
Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala	
35 40 45	
GGC CTC CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC	479
Gly Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr	
50 55 60	
CAC CGA GGG TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG	524
His Arg Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu	
65 70 75	
AAA ACT GGT GAG ACA ATA AAT GAC GCT GTG CTC TGT GCC GTG GGG	569
Lys Thr Gly Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly	
80 85 90	
ATC GTC ATT GCC ATC CTC GCG ATC ATC ACG GGG GAA TTC TAC CGG	614
Ile Val Ile Ala Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg	
95 100 105	
ATC TAT TAC CTG AAG AAG TCG CGG TCG ACG ATT CAG AAC CCC TAC	659
Ile Tyr Tyr Leu Lys Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr	
110 115 120	
GTG GCA GCA CTC TAT AAG CAA GTG GGC TGC TTC CTC TTT GGC TGT	704
Val Ala Ala Leu Tyr Lys Gln Val Gly Cys Phe Leu Phe Gly Cys	
125 130 135	
GCC ATC AGC CAG TCT TTC ACA GAC ATT GCC AAA GTG TCC ATA GGG	749
Ala Ile Ser Gln Ser Phe Thr Asp Ile Ala Lys Val Ser Ile Gly	
140 145 150	
CGC CTG CGT CCT CAC TTC TTG AGT GTC TGC AAC CCT GAT TTC AGC	794
Arg Leu Arg Pro His Phe Leu Ser Val Cys Asn Pro Asp Phe Ser	
155 160 165	
CAG ATC AAC TGC TCT GAA GGC TAC ATT CAG AAC TAC AGA TGC AGA	839
Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln Asn Tyr Arg Cys Arg	
170 180	
GGT GAT GAC AGC AAA GTC CAG GAA GCC AGG AAG TCC TTC TTC TCT	884
Gly Asp Asp Ser Lys Val Gln Glu Ala Arg Lys Ser Phe Phe Ser	
185 190 195	
GGC CAT GCC TCC TCC ATG TAC ACT ATG CTG TAT TTG GTG CTA	929
Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr Leu Val Leu	
200 205 210	
TAC CTG CAG GCC CGC TTC ACT TGG CGA GGA GCC CGC CTG CTC CGG	974
Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu Leu Arg	
215 220 225	
CCC CTC CTG CAG TTC ACC TTG ATC ATG ATG GCC TTC TAC ACG GGA	1019
Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr Thr Gly	
230 235 240	
CTG TCT CGC GTA TCA GAC CAC AAG CAC CAT CCC AGT GAT GTT CTG	1064
Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val Leu	
245 250 255	
GCA GGA TTT GCT CAA GGA GCC CTG GTG GCC TGC TGC ATA GTT TTC	1109
Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe	

Continuation of Figure 3

260	265	270	
TTC GTG TCT GAC CTC TTC AAG ACT AAG ACG ACG CTC TCC CTG CCT			1154
Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro			
275	280	285	
GCC CCT GCT ATC CGG AAG GAA ATC CTT TCA CCT GTG GAC ATT ATT			1199
Ala Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile			
290	295	300	
GAC AGG AAC AAT CAC CAC AAC ATG ATG TAG GTGCCACCCACCTCCTGAGC			1249
Asp Arg Asn Asn His His Asn/Met Met ***			
305	310		
TGTTTTGTAAAATGACTGCTGACAGCAAGTTCTTGCTGCTCTCCAATCTCATCAGACAG			1309
TAGAATGTAGGGAAAAACTTTGCCGACTGATTTAAAAAAAAAAAAAA			1362

Figure 4. Translated sequence of human PAP- $\gamma$  cDNA

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTG CTG TGC Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys	47
5 10	
TTA CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC Leu Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn	92
15 20 25	
GCC CCG TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG Ala Pro Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg	137
30 35 40	
TAC CCC TAC CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG Tyr Pro Tyr Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly	182
45 50 55	
TAC ACC ATC ACG GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC Val Thr Ile Thr Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala	227
60 65 70	
TAC CTG GTG TAC ACA GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC Tyr Leu Val Tyr Thr Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn	272
75 80 85	
AAC TAC GTG GCT GCT GTA TAC AAG GTG CTG GGG ACC TTC CTG TTT Asn Tyr Val Ala Ala Val Tyr Lys Val Leu Gly Thr Phe Leu Phe	317
90 95 100	
Gly Ala Ala Val Ser Gln Ser Leu Thr Asp Leu Ala Lys Tyr Met	362
105 110 115	
ATT GGG CGT CTG AAG CCC AAC TTC CTA GCC GTC TGC GAC CCC GAC Ile Gly Arg Leu Lys Pro Asn Phe Leu Ala Val Cys Asp Pro Asp	407
120 125 130	
TGG AGC CGG GTC AAC TGC TCG GTC TAT GTG CAG CTG GAG AAG GTG Trp Ser Arg Val Asn Cys Ser Val Tyr Val Gln Leu Glu Lys Val	452
135 140 145	
TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG GCC AGG TTG TCT TTC Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala Arg Leu Ser Phe	497
150 155 160	
TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC ATG GTG TTC TTG Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met Val Phe Leu	542
165 170 175	
GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG GCA CGG CTG Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala Arg Leu	587
180 185 190	
CTG CGA CCC ACA GTC CAG TTC CTG GTG GCC TTT GCC CTC TAC Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu Tyr	632
195 200 205	
GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC GAT Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp	677
210 215 220	
GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	722
225 230 235	
GTC TGC TAC ATC TCA GAC TTC AAA GCC CGA CCC CCA CAG CAC Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His	767
240 245 250	
TGT CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG Cys Leu Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu	812
255 260 265	
ACG TTG ACC CTG GGG CGA GGC TGA CCACAACCACTTATGGGATACCCGCACT Thr Leu Thr Leu Gly Arg Gly ***	864
270 275	
CTTCTTCCCTGAGGCCGGACCCCCCCCAGGCAGGGAGCTGCTGTGAGTCCAGCTGATGCC ACCCAGGTGGTCCCTCCAGCCTGGTTAGGCAGGGTCTGGACGGGCTCCAGGAACC	924
	984

Continuation of Figure 4

CTGGGCTGATGGGAGCAGTGAGCGGTTCCGCTGCCCTGCACGGACCAGGAGT	1044
CTGGAGATGCCTGGGTAGCCCTCAGCATTGGAGGGAACCTGTTCCCGTCGGTCCCCAA	1104
ATATCCCCCTCTTTTATGGGGTTAAGGAAGGGACCGAGAGATCAGATAGTTGCTGTTT	1164
GTAAAATGTAATGTATATGTGGTTTAGTAAAATAGGGCACCTGTTCACAAAAAA	1224
AAAAAAAAAA	1234

Figure 5. Amino acid sequences alignment of murine PAP with the three human isoforms of PAP.

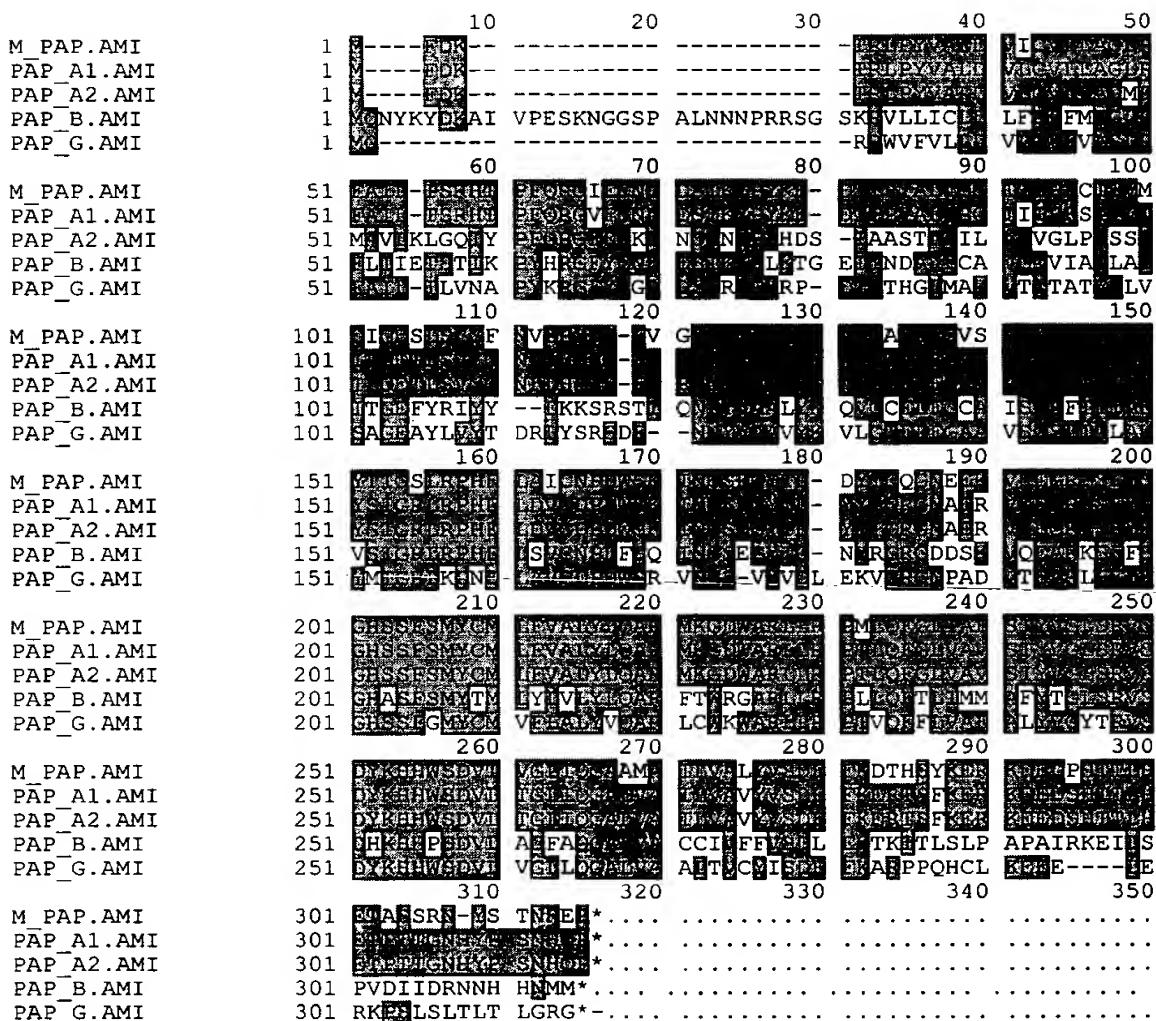


Figure 6.

Expression of PAP- $\beta$  induced with IL-1 $\beta$  in ECV304 Cells

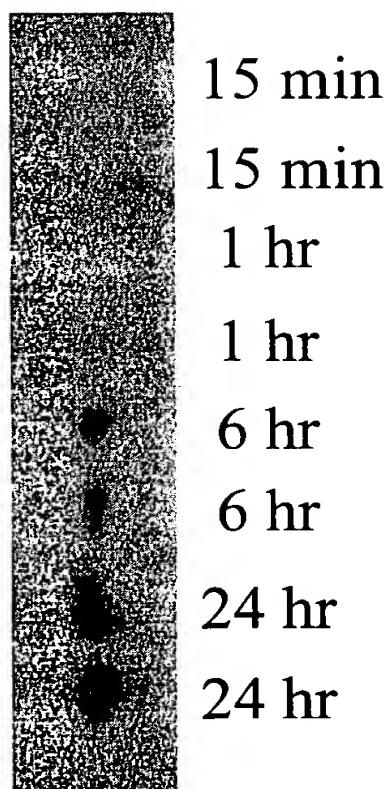
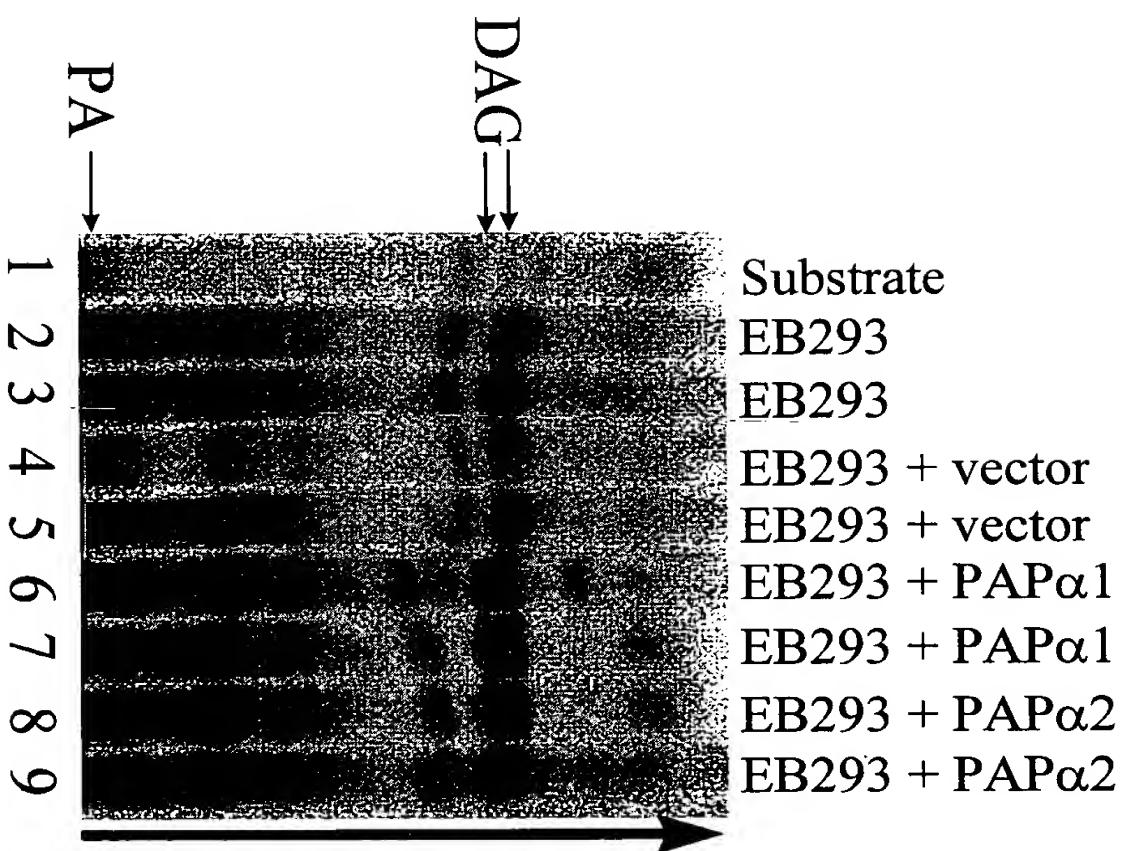


Figure 7



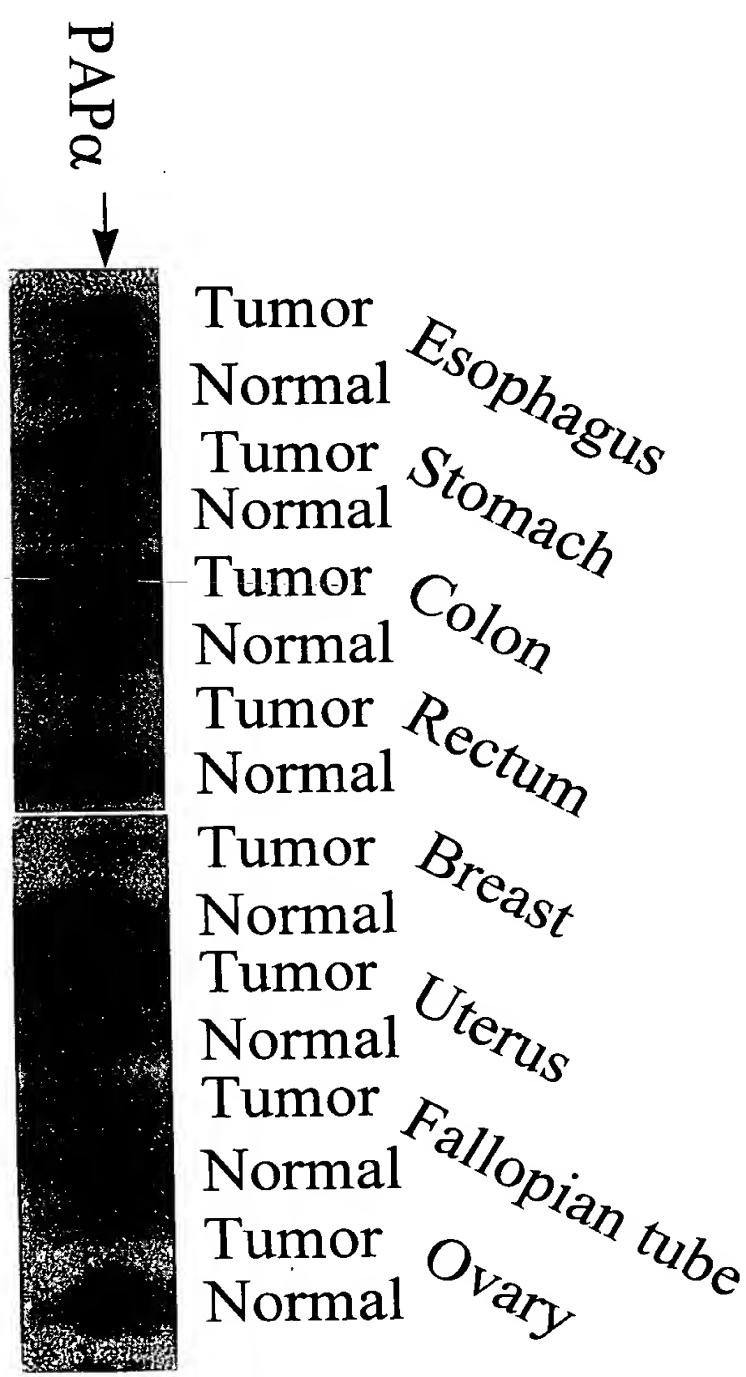


Fig. 8 Northern Analysis of PAP- $\alpha$  mRNA expression in tumor vs normal tissues

FIGURE 9

